

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Shah, Purvi

(ii) TITLE OF THE INVENTION: NOVEL TUMOR SUPPRESSOR

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
- (B) STREET: 3174 Porter Drive
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To Be Assigned
- (B) FILING DATE: Filed Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Billings, Lucy J.
- (B) REGISTRATION NUMBER: 36,749
- (C) REFERENCE/DOCKET NUMBER: PF-0249 US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415-855-0555
- (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THPINOT03
- (B) CLONE: 2446131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Tyr	Lys	Pro	Ile	Ala	Pro	Ala	Pro	Ser	Xaa	Thr	Pro	Gly	Ser
1				5					10					15	
Ser	Thr	Pro	Gly	Pro	Gly	Thr	Pro	Val	Pro	Thr	Gly	Ser	Val	Pro	Ser
			20					25					30		
Pro	Ser	Gly	Ser	Val	Pro	Gly	Ala	Gly	Ala	Pro	Phe	Arg	Pro	Leu	Phe
			35				40				45				
Asn	Asp	Phe	Gly	Pro	Pro	Ser	Met	Gly	Tyr	Val	Gln	Ala	Met	Lys	Pro

50		55		60
Pro Gly Ala Gln Gly Ser Gln Ser Thr Tyr Thr		Asp Leu Leu Ser Val		
65		70		75
Ile Glu Glu Met Gly Lys Glu Ile Arg Pro Thr Tyr Ala Gly Ser Lys				80
		85		90
Ser Ala Met Glu Arg Leu Lys Arg Gly Ile Ile His Ala Arg Ala Leu				95
		100		105
Val Arg Glu Cys Leu Ala Glu Thr Glu Arg Asn Ala Arg Thr				110
		115		120
				125

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 667 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THPINOT03
- (B) CLONE: 2446131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTGAGCGG	CCCCGAGCC	AACCCCGAG	GAGCGGCCGG	CTGGCGTCCG	CCGCGCCAG	60
GAGTTGGGGA	TGTCCTACAA	ACCCATCGCC	CCTGCTCCCA	GCAKCACCCC	TGGCTCCAGC	120
ACCCCTGGGC	CGGGCACCCC	GGTCCCTACA	GGAAGCGTCC	CGTCGCCGTC	GGGCTCAGTG	180
CCAGGAGCCG	GCGCTCCTTT	CAGACCGCTG	TTTAACGACT	TTGGACCGCC	TTCCATGGGC	240
TACGTGCAGG	CGATGAAGCC	ACCCGCGGCC	CAGGGCTCCC	AGAGCACCTA	CACGGACCTG	300
CTGTCACTCA	TAGAGGAGAT	GGGCAAAGAG	ATCCGGCCTA	CCTATGCTGG	CAGCAAGAGC	360
GCCATGGAGC	GCCTGAAGAG	AGGTATCATC	CATGCCCCGG	CCCTAGTCAG	AGAGTGCCTG	420
GCAGAGACAG	AGCGGAACGC	CCGCACGTAA	CAGGAAGCGC	CTCGGCCTCA	GCGTCTGGAC	480
CTATCCGGCC	ACTGCAGAGC	ACCCGCTTCT	CCCTGGCCTT	CATCCCGAGT	TGCACTAACC	540
ATCCTGGGCT	TCCTGTCCTG	TGTCCCTTGG	TGGGTCCCCT	CCAGGAACCA	AGGAGTGGCC	600
CTCCAGGTGG	CAGCACTAAG	GACACCCCCC	CACAACAAGA	GTTAGCAGCG	AGGTCCCCAT	660
GAGTCCC						667

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 606837

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Tyr Lys Pro Asn Leu Thr Ala His Met Pro Ala Ala Ala Leu														
1				5				10					15	
Asn Ala Gly Ser Val His Ser Pro Ser Thr Ser Met Ala Thr Ser Ser														
			20					25				30		
Gln Tyr Arg Gln Leu Leu Ser Asp Tyr Gly Pro Pro Ser Leu Gly Tyr														
			35					40				45		
Thr Gln Gly Thr Gly Asn Ser Gln Val Pro Gln Ser Lys Tyr Ala Glu														
			50					55				60		
Leu Leu Ala Ile Ile Glu Glu Leu Gly Lys Glu Ile Arg Pro Thr Tyr														
			65					70				75		80
Ala Gly Ser Lys Ser Ala Met Glu Arg Leu Lys Arg Gly Ile Ile His														
			85					90				95		
Ala Arg Ser Leu Val Arg Glu Cys Leu Ala Glu Thr Glu Arg Asn Ala														
			100					105				110		
Arg Ser														